

SEQUENCE LISTING

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Park, Jason
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<120> Compositions And Methods For Identifying And Targeting Cancer Cells Of Alimentary Canal Origin

<130> TJU2412

<150> 60/192,229

<151> 2000-03-27

<160> 2

<170> PatentIn version 3.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

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Pro Gly Trp Leu Ser Phe Ser Ser Gln Val Ser Gln Asn Cys His Asn	
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ggc agc tat gaa atc agc gtc ctg atg atg ggc aac tca gcc ttt gca	261
Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala	
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Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile	
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Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala	
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act ttc atg tat tcg gat ggt ctg att cat aac tca ggc gac tgc cgg	405
Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg	
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agt agc acc tgt gaa ggc ctc gac cta ctc agg aaa att tca aat gca	453
Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala	
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Asn Ser Lys Leu Pro Asn Asp Ile Thr Gly Arg Gly Pro Gln Ile Leu	420	425	430	
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Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu	435	440	445	
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Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg	450	455	460	
cag aaa aaa tgg tcc cac att cct cct gaa aat atc ttt cct ctg gag				1557
Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu	465	470	475	480
acc aat gag acc aat cat gtt agc ctc aag atc gat gat gac aaa aga				1605
Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg	485	490	495	
cga gat aca atc cag aga cta cga cag tgc aaa tac gtc aaa aag cga				1653
Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Val Lys Lys Arg	500	505	510	
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Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys	515	520	525	
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Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Ile Asp Tyr Tyr Thr Leu	530	535	540	
acc aag ttc tac ggg aca gtg aaa ctg gat acc atg atc ttc ggg gtg				1797
Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val	545	550	555	560
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Ile Glu Tyr Cys Glu Arg Gly Ser Leu Arg Glu Val Leu Asn Asp Thr	565	570	575	
att tcc tac cct gat ggc aca ttc atg gat tgg gag ttt aag atc tct				1893
Ile Ser Tyr Pro Asp Gly Thr Phe Met Asp Trp Glu Phe Lys Ile Ser	580	585	590	
gtc ttg tat gac att gct aag gga atg tca tat ctg cac tcc agt aag				1941
Val Leu Tyr Asp Ile Ala Lys Gly Met Ser Tyr Leu His Ser Ser Lys	595	600	605	
aca gaa gtc cat ggt cgt ctg aaa tct acc aac tgc gta gtg gac agt				1989
Thr Glu Val His Gly Arg Leu Lys Ser Thr Asn Cys Val Val Asp Ser	610	615	620	
aga atg gtg gtg aag atc act gat ttt ggc tgc aat tcc att ttg cct				2037
Arg Met Val Val Lys Ile Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro	625	630	635	640
cca aaa aag gac ctg tgg aca gct cca gag cac ctc cgc caa gcc aac				2085
Pro Lys Lys Asp Leu Trp Thr Ala Pro Glu His Leu Arg Gln Ala Asn	645	650	655	

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aat gag aag att ttc aga gtg gaa aat tcc aat gga atg aaa ccc ttc Asn Glu Lys Ile Phe Arg Val Glu Asn Ser Asn Gly Met Lys Pro Phe 690 695 700	2229
cgc cca gat tta ttc ttg gaa aca gca gag gaa aaa gag cta gaa gtg Arg Pro Asp Leu Phe Leu Glu Thr Ala Glu Lys Glu Leu Glu Val 705 710 715 720	2277
tac cta ctt gta aaa aac tgt tgg gag gaa gat cca gaa aag aga cca Tyr Leu Leu Val Lys Asn Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro 725 730 735	2325
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cat gac caa aaa aat gaa agc tat atg gat acc ttg atc cga cgt cta His Asp Gln Lys Asn Glu Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu 755 760 765	2421
cag cta tat tct cga aac ctg gaa cat ctg gta gag gaa agg aca cag Gln Leu Tyr Ser Arg Asn Leu Glu His Leu Val Glu Glu Arg Thr Gln 770 775 780	2469
ctg tac aag gca gag agg gac agg gct gac aga ctt aac ttt atg ttg Leu Tyr Lys Ala Glu Arg Asp Arg Ala Asp Arg Leu Asn Phe Met Leu 785 790 795 800	2517
ctt cca agg cta gtg gta aag tct ctg aag gag aaa ggc ttt gtg gag Leu Pro Arg Leu Val Val Lys Ser Leu Lys Glu Lys Gly Phe Val Glu 805 810 815	2565
ccg gaa cta tat gag gaa gtt aca atc tac ttc agt gac att gta ggt Pro Glu Leu Tyr Glu Glu Val Thr Ile Tyr Phe Ser Asp Ile Val Gly 820 825 830	2613
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gtc tac aag gtg gaa acc atc ggt gat gcg tac atg gtg gct agt ggt Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met Val Ala Ser Gly 865 870 875 880	2757
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2412.ST25

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gct gct gga gtt gtg gga atc aag atg cct cgt tat tgt cta ttt gga 2949
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 Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Thr Gly Leu Pro Leu
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 Arg Ile His Val Ser Gly Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu
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 Asn Leu Pro Thr Pro Pro Thr Val Glu Asn Gln Gln Arg Leu Gln
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 Lys Lys Gly Thr Leu Glu Tyr Leu Gln Leu Asn Thr Thr Asp Lys
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 Glu Ser Thr Tyr Phe
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Gly Ser Tyr Glu Ile Ser Val Leu Met Met Gly Asn Ser Ala Phe Ala
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Glu Pro Leu Lys Asn Leu Glu Asp Ala Val Asn Glu Gly Leu Glu Ile
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Val Arg Gly Arg Leu Gln Asn Ala Gly Leu Asn Val Thr Val Asn Ala
65 70 75 80

Thr Phe Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg
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Ser Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
100 105 110

Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr
115 120 125

Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala
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Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu
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Met Ser Pro Ala Arg Lys Leu Met Tyr Phe Leu Val Asn Phe Trp Lys
165 170 175

Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val
180 185 190

Tyr Lys Asn Gly Thr Glu Thr Glu Asp Cys Phe Trp Tyr Leu Asn Ala
195 200 205

Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
210 215 220

Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn
225 230 235 240

Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr
245 250 255

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Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro
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Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Asn Ser
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Leu Leu Asn Ser Ser Phe Ser Arg Asn Leu Ser Pro Thr Lys Arg Asp
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Phe Arg Leu Ala Tyr Leu Asn Gly Ile Leu Val Phe Gly His Met Leu
 325 330 335

Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro Lys Phe Ala
 340 345 350

His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp Gly Pro Val Thr
 355 360 365

Leu Asp Asp Trp Gly Asp Val Asp Ser Thr Met Val Leu Leu Tyr Thr
 370 375 380

Ser Val Asp Thr Lys Lys Tyr Lys Val Leu Leu Thr Tyr Asp Thr His
 385 390 395 400

Val Asn Lys Thr Tyr Pro Val Asp Met Ser Pro Thr Phe Thr Trp Lys
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Asn Ser Lys Leu Pro Asn Asp Ile Thr Gly Arg Gly Pro Gln Ile Leu
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Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu
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Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg
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Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu
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Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg
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Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys

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515

520

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565 570 575

Ile Ser Tyr Pro Asp Gly Thr Phe Met Asp Trp Glu Phe Lys Ile Ser
580 585 590

Val Leu Tyr Asp Ile Ala Lys Gly Met Ser Tyr Leu His Ser Ser Lys
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Thr Glu Val His Gly Arg Leu Lys Ser Thr Asn Cys Val Val Asp Ser
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Arg Met Val Val Lys Ile Thr Asp Phe Gly Cys Asn Ser Ile Leu Pro
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Pro Lys Lys Asp Leu Trp Thr Ala Pro Glu His Leu Arg Gln Ala Asn
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Ile Ser Gln Lys Gly Asp Val Tyr Ser Tyr Gly Ile Ile Ala Gln Glu
660 665 670

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675 680 685

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Tyr Leu Leu Val Lys Asn Cys Trp Glu Glu Asp Pro Glu Lys Arg Pro
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Asp Phe Lys Lys Ile Glu Thr Thr Leu Ala Lys Ile Phe Gly Leu Phe
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His Asp Gln Lys Asn Glu Ser Tyr Met Asp Thr Leu Ile Arg Arg Leu
755 760 765

Gln Leu Tyr Ser Arg Asn Leu Glu His Leu Val Glu Glu Arg Thr Gln
770 775 780

Leu Tyr Lys Ala Glu Arg Asp Arg Ala Asp Arg Leu Asn Phe Met Leu
785 790 795 800

Leu Pro Arg Leu Val Val Lys Ser Leu Lys Glu Lys Gly Phe Val Glu
805 810 815

Pro Glu Leu Tyr Glu Glu Val Thr Ile Tyr Phe Ser Asp Ile Val Gly
820 825 830

Phe Thr Thr Ile Cys Lys Tyr Ser Thr Pro Met Glu Val Val Asp Met
835 840 845

Leu Asn Asp Ile Tyr Lys Ser Phe Asp His Ile Val Asp His His Asp
850 855 860

Val Tyr Lys Val Glu Thr Ile Gly Asp Ala Tyr Met Val Ala Ser Gly
865 870 875 880

Leu Pro Lys Arg Asn Gly Asn Arg His Ala Ile Asp Ile Ala Lys Met
885 890 895

Ala Leu Glu Ile Leu Ser Phe Met Gly Thr Phe Glu Leu Glu His Leu
900 905 910

Pro Gly Leu Pro Ile Trp Ile Arg Ile Gly Val His Ser Gly Pro Cys
915 920 925

Ala Ala Gly Val Val Gly Ile Lys Met Pro Arg Tyr Cys Leu Phe Gly
930 935 940

Asp Thr Val Asn Thr Ala Ser Arg Met Glu Ser Thr Gly Leu Pro Leu
945 950 955 960

Arg Ile His Val Ser Gly Ser Thr Ile Ala Ile Leu Lys Arg Thr Glu
965 970 975

Cys Gln Phe Leu Tyr Glu Val Arg Gly Glu Thr Tyr Leu Lys Gly Arg
980 985 990

Gly Asn Glu Thr Thr Tyr Trp Leu Thr Gly Met Lys Asp Gln Lys Phe
995 1000 1005

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Ala Glu Phe Ser Asp Met Ile Ala Asn Ser Leu Gln Lys Arg Gln
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Lys Lys Gly Thr Leu Glu Tyr Leu Gln Leu Asn Thr Thr Asp Lys
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Glu Ser Thr Tyr Phe
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